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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/873,881	06/04/2001	Fred W. Scott	18617.NEW

CONFIRMATION NO. 6373
FORMALITIES LETTER



OC00000007141372

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Date Mailed: 11/30/2001

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 CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
 DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

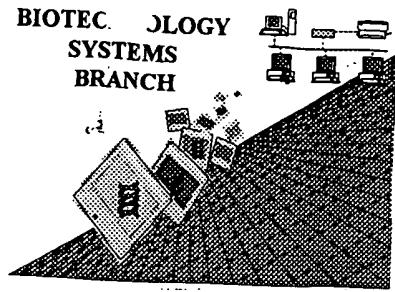
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PART 3 - OFFICE COPY

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,881A

Source: OPE

Date Processed by STIC: 10/15/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
 - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001

TIME: 15:47:14

Input Set : A:\corrected sequence listing for Scott et al
 Output Set: N:\CRF3\10152001\I873881A.raw

3 <110> APPLICANT: Scott, Fred W.
 5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
 7 <130> FILE REFERENCE: 18617.0016
 9 <140> CURRENT APPLICATION NUMBER: US 09/873,881A
 10 <141> CURRENT FILING DATE: 2001-06-04
 12 <150> PRIOR APPLICATION NUMBER: US 08/552,369
 13 <151> PRIOR FILING DATE: 1995-11-03
 15 <160> NUMBER OF SEQ ID NOS: 19

*Does Not Comply
Corrected Diskette Needed*

ERRORED SEQUENCES

932 <210> SEQ ID NO: 19
 933 <211> LENGTH: 1979
 934 <212> TYPE: DNA
 935 <213> ORGANISM: feline leukemia virus
 937 <220> FEATURE:
 938 <223> OTHER INFORMATION:
 940 <400> SEQUENCE: 19

941 accaccaatc aagacctctc ggacagcccc agtcagacg atccatcaag	50
943 atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctc	95
944 Met Glu Ser Pro Thr His Pro Ser Lys Pro Ser Lys Asp Lys Thr Leu	
945 1 5 10 15	
947 tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac	140
948 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp	
949 20 25 30	
951 ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act	185
952 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr	
953 35 40 45	
955 tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc	230
956 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr	
957 50 55 60	
959 tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt	275
960 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val	
961 65 70 75	
963 gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta	320
964 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu	
965 <i>delete</i> 80 85 90	
967 aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365
968 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys	
W--> 969 95 100 105	
971 tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410
972 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr	
973 110 115 120	
975 ccc ttt tac gtc tgc ccc gga cat gcc ccc tgg ggg cca aag	455
976 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys	
977 125 130 135	

W-->
OK
W-->

pp 1,3-4

*→ numbers are
in bold print
→ due to error
above - apostrophe*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881A

DATE: 10/15/2001

TIME: 15:47:15

Input Set : A:\corrected sequence listing for Scott et al
 Output Set: N:\CRF3\10152001\I873881A.raw

979	gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500
980	Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp	
W--> 981	140 145 150	
983	gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545
984	Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser	
W--> 985	155 160 165	
987	tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590
988	Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser	
W--> 989	170 175 180	
991	tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635
992	Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys	
W--> 993	185 190 195	
995	gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga	680
996	Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg	
W--> 997	200 205 210	
999	cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc	725
1000	Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser	
W--> 1001	215 220 225	
1003	cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac	770
1004	Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn	
W--> 1005	230 235 240	
1007	cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca	815
1008	Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr	
W--> 1009	245 250 255	
1011	ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc	860
1012	Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala	
W--> 1013	260 265 270	
1015	cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg	905
1016	Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly	
W--> 1017	275 280 285	
1019	acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc	950
1020	Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala	
W--> 1021	290 295 300	
1023	tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc	995
1024	Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys	
W--> 1025	305 310 315	
1027	ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt	1040
1028	Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly	
W--> 1029	320 325 330	
1031	acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act	1085
1032	Asn Tyr Ser Asn Gln Thr Asn Pro Pro Ser Cys Leu Ser Ile	
W--> 1033	335 340 345	
1035	ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg	1130
1036	Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met	
W--> 1037	350 355 360	
1039	tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag	1175
1040	Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys	
W--> 1041	365 370 375	
1043	aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac	1220

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1044	Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn		
W--> 1045	380	385	390
1047	ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc	1265	
1048	Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser		
W--> 1049	395	400	405
1051	atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa	1310	
1052	Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu		
W--> 1053	410	415	420
1055	tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca	1355	
1056	Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr		
W--> 1057	425	430	435
1059	cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta	1400	
1060	His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile Ser Leu		
W--> 1061	440	445	450
1063	acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc	1445	
1064	Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala		
W--> 1065	455	460	465
1067	gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gca cag	1490	
1068	Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln		
W--> 1069	470	475	480
1071	tcc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta	1535	
1072	Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu		
W--> 1073	485	490	495
1075	gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct	1580	
1076	Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser		
W--> 1077	500	505	510
1079	gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta	1625	
1080	Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu		
W--> 1081	515	520	525
1083	caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc	1670	
1084	Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe		
W--> 1085	530	535	540
1087	tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta	1715	
1088	Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu		
W--> 1089	545	550	555
1091	aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag	1760	
1092	Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln		
W--> 1093	560	565	570
1095	gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc	1805	
1096	Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr		
W--> 1097	575	580	585
1099	cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att	1850	
1100	Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile		
W--> 1101	590	595	600
1103	ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta	1895	
1104	Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val		
W--> 1105	605	610	615
1107	aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag	1940	
W--> 1108	Lys Asp Axg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln		

*Muahid**T*

RAW SEQUENCE LISTING

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W--> 1109

620

625

630

1111 tac caa cag ata aag caa tac gat ccg gac cga cca tga
1112 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro

1979

W--> 1113

635

640

E--> 1117 bFLOdOcs:589477_1 (cm%d01)

delete

VERIFICATION SUMMARY DATE: 10/15/2001
PATENT APPLICATION: US/09/873,881A TIME: 15:47:16

Input Set : A:\corrected sequence listing for Scott et al
Output Set: N:\CRF3\10152001\I873881A.raw

L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:912 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:989 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:993 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:997 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1001 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:1117 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1995 SEQ:19
L:1117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
L:1117 M:112 C: (48) String data converted to lower case,
L:1117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1995 SEQ:19